



SEQUENCE LISTING

<110> Sheppard, Paul O.

<120> IL-28 AND IL-29 TRUNCATED CYSTEINE
MUTANTS AND METHODS OF USING SAME

<130> 05-22P1

<160> 150

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(618)

<221> misc_fe

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 1 5 10 15
 acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct ctc ccg 96
 Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala Leu Pro
 20 25 30

26 gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
35 40 45

gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
50 55 60

gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg gag gct
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala
85 90 95

gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 35
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp.
 100 105 110
 100

cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg cac cat
 Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125

atc ctc tcc cag ttc cg^g gcc tgt gtg agt cgt cag ggc ctg gg^c acc
 Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr
 130 135 140

cag atc cag cct cag ccc acg gca ggg ccc agg acc acc cggtt ggc cgcc ctc 4

Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu			
145	150	155	160
cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag tcc cct			528
His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro			
165	170	175	
ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg			576
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr			
180	185	190	
cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga			618
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *			
195	200	205	

<210> 2
<211> 205
<212> PRT
<213> Homo sapiens

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Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala Val Leu			
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Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala Leu Pro			
20	25	30	
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln			
35	40	45	
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu			
50	55	60	
Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp			
65	70	75	80
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala			
85	90	95	
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp			
100	105	110	
Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His			
115	120	125	
Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr			
130	135	140	
Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu			
145	150	155	160
His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro			
165	170	175	
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr			
180	185	190	
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val			
195	200	205	

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<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(603)

<221> misc_feature
<222> (0)...(0)
<223> IL-29

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 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
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 gcc gtc gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag 96
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys
 20 25 30
 ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg 144
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
 35 40 45
 agc ttg aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa 192
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys
 50 55 60
 aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg 240
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 65 70 75 80
 ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc 288
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 85 90 95
 ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac 336
 Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp
 100 105 110
 gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc 384
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 115 120 125
 cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc 432
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
 130 135 140
 cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag 480
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 145 150 155 160
 tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc 528
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 165 170 175
 ctc acg cga gac ctc aaa tat gtg gcc gat ggg gac ctg tgt ctg aga 576
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg
 180 185 190
 acg tca acc cac cct gag tcc acc tga 603
 Thr Ser Thr His Pro Glu Ser Thr *
 195 200

<210> 4
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 4
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 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
 35 40 45

Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
 50 55 60
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 65 70 75 80
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 85 90 95
 Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
 100 105 110
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 115 120 125
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
 130 135 140
 Arg Leu His His Trp Leu His Arg Leu Gln Ala Pro Lys Lys Glu
 145 150 155 160
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 165 170 175
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg
 180 185 190
 Thr Ser Thr His Pro Glu Ser Thr
 195 200

<210> 5
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 <212> DNA
 <213> Homo sapiens

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 <222> (1)....(615)

 <221> misc_feature
 <222> (0)....(0)
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 1 5 10 15
 acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg 96
 Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro
 20 25 30
 gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
 35 40 45
 gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
 50 55 60
 ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg 240
 Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp
 65 70 75 80
 gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct 288
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala
 85 90 95
 gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 336
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
 100 105 110
 cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg cac cat 384

Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125

atc ctc tcc cag ctc cgg gcc tgc ttt agt cgt cag ggc ccg ggc acc 432
 Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr
 130 135 140

cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc 480
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
 145 150 155 160

cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
 165 170 175

ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 576
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 180 185 190

cga gac ctg aat tgg gtt gcc agc ggg gac ctg tgg gtc 615
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 195 200

<210> 6
<211> 205
<212> PRT
<213> Homo sapiens

<400> 6
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 Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro
 20 25 30
 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
 35 40 45
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
 50 55 60
 Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp
 65 70 75 80
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala
 85 90 95
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
 100 105 110
 Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125
 Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr
 130 135 140
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
 145 150 155 160
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
 165 170 175
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 180 185 190
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 195 200 205

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<212> DNA
<213> Mus musculus

<220>
<221> CDS

<222> (22)...(630)

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ctc ctc ctg ctg ttg cct ctg ctg gcc gca gtg ctg aca aga acc 99
 Leu Leu Leu Leu Leu Pro Leu Leu Ala Ala Val Leu Thr Arg Thr
 15 20 25

caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag 147
 Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys
 30 35 40

gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag 195
 Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln
 45 50 55

gcc ttc aaa aag gcc aag gat gcc atc gag aag agg ctg ctt gag aag 243
 Ala Phe Lys Lys Ala Lys Asp Ala Ile Glu Lys Arg Leu Glu Lys
 60 65 70

gac ctg agg tgc agt tcc cac ctc ttc ccc agg gcc tgg gac ctg aag 291
 Asp Leu Arg Cys Ser Ser His Leu Phe Pro Arg Ala Trp Asp Leu Lys
 75 80 85 90

cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc 339
 Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala
 95 100 105

ctg acc ctg aag gtc tgg gag aac atg act gac tca gcc ctg gcc acc 387
 Leu Thr Leu Lys Val Trp Glu Asn Met Thr Asp Ser Ala Leu Ala Thr
 110 115 120

atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg 435
 Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu
 125 130 135

cag acc tgt aca cag ctt cag gcc aca gca gag ccc agg tcc ccg agc 483
 Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser
 140 145 150

cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag 531
 Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys
 155 160 165 170

gag acc cct ggc tgc ctg gag gcc tct gtc acc tcc aac ctg ttt cgc 579
 Glu Thr Pro Gly Cys Leu Glu Ala Ser Val Thr Ser Asn Leu Phe Arg
 175 180 185

ctg ctc acc cgg gac ctc aag tgt gtg gcc aat gga gac cag tgt gtc 627
 Leu Leu Thr Arg Asp Leu Lys Cys Val Ala Asn Gly Asp Gln Cys Val
 190 195 200

tga cct 633
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<210> 8
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<212> PRT
<213> Mus musculus

<400> 8
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 20 25 30
 Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln
 35 40 45
 Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys
 50 55 60
 Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Leu Arg Cys Ser Ser
 65 70 75 80
 His Leu Phe Pro Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu
 85 90 95
 Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp
 100 105 110
 Glu Asn Met Thr Asp Ser Ala Leu Ala Thr Ile Leu Gly Gln Pro Leu
 115 120 125
 His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu
 130 135 140
 Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser Arg Arg Leu Ser Arg Trp
 145 150 155 160
 Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu
 165 170 175
 Glu Ala Ser Val Thr Ser Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
 180 185 190
 Lys Cys Val Ala Asn Gly Asp Gln Cys Val
 195 200

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<211> 632
<212> DNA
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<220>
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<222> (22) ... (630)

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ctc ctc ctg ttg cct ctg ctg gcc gca gtg ctg aca aga acc 99
Leu Leu Leu Leu Pro Leu Leu Ala Ala Val Leu Thr Arg Thr
 15 20 25
caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag 147
Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys
 30 35 40
gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag 195
Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln
 45 50 55
gcc ttc aaa aag gcc aag ggt gcc atc gag aag agg ctg ctt gag aag 243
Ala Phe Lys Lys Ala Lys Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys
 60 65 70
gac atg agg tgc agt tcc cac ctc atc tcc agg gcc tgg gac ctg aag 291
Asp Met Arg Cys Ser Ser His Leu Ile Ser Arg Ala Trp Asp Leu Lys
 75 80 85 90
cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gag gct gag gtg gcc 339
Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala

95	100	105	
ctg acc ctg aag gtc tgg gag aac ata aat gac tca gcc ctg acc acc Leu Thr Leu Lys Val Trp Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr 110 115 120			387
atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu 125 130 135			435
cag acc tgt aca cag ctt cag gcc aca gca gag ccc aag ccc ccg agt Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser 140 145 150			483
cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys 155 160 165 170			531
gag act cct ggc tgc ctg gag gac tct gtc acc tcc aac ctg ttt caa Glu Thr Pro-Gly-Cys-Leu Glu Asp Ser Val Thr Ser Asn Leu Phe Gln 175 180 185			579
ctg ctc ctc cgg gac ctc aag tgt gtg gcc agt gga gac cag tgt gtc Leu Leu Arg Asp Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val 190 195 200			627
tga cc			632
*			
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1 5 10 15			
Leu Leu Leu Ala Ala Val Leu Thr Arg Thr Gln Ala Asp Pro Val Pro 20 25 30			
Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln 35 40 45			
Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys 50 55 60			
Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Met Arg Cys Ser Ser 65 70 75 80			
His Leu Ile Ser Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu 85 90 95			
Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp 100 105 110			
Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr Ile Leu Gly Gln Pro Leu 115 120 125			
His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu 130 135 140			
Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser Arg Arg Leu Ser Arg Trp 145 150 155 160			
Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu 165 170 175			
Glu Asp Ser Val Thr Ser Asn Leu Phe Gln Leu Leu Leu Arg Asp Leu 180 185 190			
Lys Cys Val Ala Ser Gly Asp Gln Cys Val 195 200			

<210> 11
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1563)

<221> misc_feature
<222> (0)...(0)
<223> IL-28RA

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gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu 20 25 30	96
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly 35 40 45	144
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr 50 55 60	192
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu 65 70 75 80	240
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe 85 90 95	288
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val 100 105 110	336
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag cgg gcc cca cct Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro 115 120 125	384
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr 130 135 140	432
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val 145 150 155 160	480
gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr 165 170 175	528
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu 180 185 190	576
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys 195 200 205	624

tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa 672
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta 720
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
 gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc 768
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 tgg ttt cag cgg gca aag atg cca cgg gcc ctg gac ttt tct gga cac 816
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
 aca cac cct gtc gca acc ttt cag ccc agc aga cca gag tcc gtg aat 864
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
 gac ttg ttc ctc tgt ccc caa aag gaa ctg acc aga ggg gtc agg ccg 912
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
 acg cct cga gtc agg gcc cca acc caa cag aca aga tgg aag aag 960
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
 gac ctt gca gag gac gaa gag gag gat gag gag gac aca gaa gat 1008
 Asp Leu Ala Glu Asp Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335
 ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc ctg ggg caa 1056
 Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg gac tca ggg 1104
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365
 agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct gct tgg gat 1152
 Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc tgg gac agg 1200
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg 1248
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415
 ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag 1296
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Glu Phe Ser Lys
 420 425 430 435
 gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg 1344
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asn Leu Ser Ser Trp
 440 445
 gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga 1392
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460

ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct 1440
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg 1488
 Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 ggc agc tgg ggg gct gag agc acc cag agg acc gac agg ggc cgg 1536
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 aca ttg ggg cat tac atg gcc agg tga 1563
 Thr Leu Gly His Tyr Met Ala Arg *
 515 520

<210> 12
<211> 520
<212> PRT
<213> Homo sapiens

<400> 12
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln 15
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His 260 265 270
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn 275 280 285
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro 290 295 300
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys 305 310 315 320
 Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp 325 330 335

Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365
 Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 Thr Leu Gly His Tyr Met Ala Arg
 515 520

<210> 13
 <211> 1476
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1) ... (1476)

 <221> misc_feature
 <222> (0) ... (0)
 <223> IL-28RA splice variant

<400> 13
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Gln
 1 5 10 15
 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336

Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110

gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg 432
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140

tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg 480
 Tyr Gln Leu Pro Pro Cys Met Pro Leu Phe Leu Lys Tyr Glu Val
 145 150 155 160

gca ttt tgg ggg ggg ggg gca acc aag acc cta ttt cca gtc act 528
 Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr
 165 170 175

ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa 576
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190

cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa 624
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205

672
 tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220

720
 gcc aac tgg gct ttc ctg gtg cca tcg ctt ctg ata ctg ctg tta
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu
 225 230 235 240

768
 gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255

816
 tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly
 260 265 270

864
 gtc agg ccg acg cct cga gtc agg gcc cca acc caa cag aca aga
 Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg
 275 280 285

912
 tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac
 Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Asp Glu Asp
 290 295 300

960
 aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc
 Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe
 305 310 315 320

1008
 ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg
 Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val
 325 330 335

1056
 gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct
 Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser
 340 345 350

1104
 gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc
 Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser

355	360	365	
tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly 370 375 380 1152			
caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu 385 390 395 400 1200			
ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu 405 410 415 1248			
tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val 420 425 430 1296			
cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu 435 440 445 1344			
agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac Ser Ser Pro Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp 450 455 460 1392			
agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp 465 470 475 1440			
agg ggc cgg aca ttg ggg cat tac atg gcc agg tga Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg * 485 490 1476			

<210> 14
<211> 491
<212> PRT
<213> Homo sapiens

<400> 14			
Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln	15		
1 5 10			
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	20 25 30		
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	35 40 45		
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	50 55 60		
Arg Arg Arg Trp Arg Glu Val Glu Cys Ala Gly Thr Lys Glu Leu	65 70 75 80		
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	85 90 95		
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	100 105 110		
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	115 120 125		
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	130 135 140		
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val	145 150 155 160		
Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr	165 170 175		
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu	180 185 190		

His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly
 260 265 270
 Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg
 275 280 285
 Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp
 290 295 300
 Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe
 305 310 315 320
 Leu Gly Gln His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val
 325 330 335
 Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser
 340 345 350
 Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser
 355 360 365
 Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
 370 375 380
 Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
 385 390 395 400
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
 405 410 415
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445
 Ser Ser Pro Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
 450 455 460
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
 465 470 475 480
 Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
 485 490

<210> 15
 <211> 674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(636)

 <221> misc_feature
 <222> (0)...(0)
 <223> IL-28RA soluble variant

<400> 15
 atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag 48
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg. 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60

cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80

cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95

aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110

gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg cca cct 384
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125

gtc ctg gtg ctc acc cag acg gag atc ctg agt gcc aat gcc acg 432
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140

tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg 480
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160

gca ttc tgg aag gag ggg ggc gga aac aag gtg gga agc tcc ttt cct 528
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175

gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc 576
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190

tca ccc tcc cag cct gct gca ccc ctc ctc cag gaa gtc ttc cct 624
 Ser Pro Ser Gln Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
 195 200 205

gta cac tcc tga cttctggcag tcagccctaa taaaatctga tcaaagta 674
 Val His Ser *
 210

<210> 16
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val

100	105	110
Glu Ser Glu Tyr Leu Asp Tyr	Leu Phe Glu Val Glu Pro	Ala Pro Pro
115	120	125
Val Leu Val Leu Thr Gln Thr	Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130	135	140
Tyr Gln Leu Pro Pro Cys Met	Pro Pro Leu Asp Leu Lys Tyr Glu Val	
145	150	155
Ala Phe Trp Lys Glu Gly Ala	Gly Asn Lys Val Gly Ser Ser Phe Pro	
165	170	175
Ala Pro Arg Leu Gly Pro Leu Leu	His Pro Phe Leu Leu Arg Phe Phe	
180	185	190
Ser Pro Ser Gln Pro Ala Pro Ala	Leu Leu Gln Glu Val Phe Pro	
195	200	205
Val His Ser		
210		

<210> 17
<211> 734
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (53)...(127)

<221> mat_peptide
<222> (128)...(655)

<221> CDS
<222> (53)...(655)

<400> 17
tgggtgacag cctcagagtg tttcttctgc tgacaaaagac cagagatcag ga atg aaa 58
Met Lys
-25

cta gac atg act ggg gac tgc acg cca gtg ctg gtg atg gcc gca 106
Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala
-20 -15 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct 154
Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala
-5 1 5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202
Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
10 15 20 25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250
Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
30 35 40

tcg ctt ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg 298
Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg
45 50 55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg 346
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu
60 65 70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
75 80 85

act gac cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg 442
 Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu
 90 95 100 105
 cac cat atc ctc tcc cag ttc cgg gcc tgt atc cag cct cag ccc acg 490
 His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr
 110 115 120
 gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg tac cgg ctc 538
 Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr Arg Leu
 125 130 135
 cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc 586
 Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val
 140 145 150
 acc ttc aac ctc ttc cgc ctc acg cga gac ctg aat tgt gtt gcc 634
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala
 155 160 165
 agt ggg gac ctg tgt gtc tga ccctcccacc agtcatgcaa cctgagattt 685
 Ser Gly Asp Leu Cys Val *
 170 175
 tatttataaa ttagccactt gtcttaattt attgcacccc agtcgctat 734

 <210> 18
 <211> 200
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> (1) ... (25)

 <400> 18
 Met Lys Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met -10
 -20 -15 -25
 Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His 5
 -5 -10 -15 -20 -25 -30 -35 -40 -45 -50 -55
 Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser 10 15 20
 Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu 25 30 35
 Glu Glu Ser Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe 40 45 50 55
 Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met 60 65 70
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr 75 80 85
 Ala Asp Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His 90 95 100
 Thr Leu His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln 105 110 115
 Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr 120 125 130 135
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala 140 145 150
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys 155 160 165
 Val Ala Ser Gly Asp Leu Cys Val 170 175

<211> 856
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (98)...(154)

<221> mat_peptide
<222> (155)...(700)

<221> CDS
<222> (98)...(700)

<400> 19
aattacctt tcactttaca cacatcatct tggattgccccc attttgcgtg gctaaaaaagc 60
agagccatgc cgctgggaa gcagttgcga tttagcc atg gct gca gct tgg acc 115
Met Ala Ala Ala Trp Thr -15

gtg gtg ctg gtg act ttg gtc cta ggc ttg gcc gtc ggc cct gtc 163
Val Val Leu Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val
-10 -5 1

ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 211
Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg
5 10 15

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 259
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
20 25 30 35

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 307
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
40 45 50

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 355
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
55 60 65

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg 403
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
70 75 80

gag gcc gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 451
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
85 90 95

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 499
His Thr Leu His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
100 105 110 115

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg 547
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
120 125 130

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag 595
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
135 140 145

gca tct gtc acc ttc aac ctc ttc cgc ctc acg cga gac ctc aaa 643
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
150 155 160

tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag 691

Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
 Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
 165 170 175

tcc acc tga caccccacac cttatttatg cgctgagccc tactcattcc 740
 Ser Thr *
 180

ttaatttatt tccttcacc ctttatttat gaagctgcag ccctgactga gacataggc 800
 tgagtttatt gtttacttt tatacattat gcacaaataa acaacaagga attgga 856

<210> 20
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(19)

<400> 20
 Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu -5
 -15 -10
 Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys 10
 1 5 10
 Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
 15 20 25
 Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys 45
 30 35 40
 Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg 60
 50 55
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala 75
 65 70
 Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp 90
 80 85
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu 105
 95 100
 Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly 125
 110 115 120
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu 140
 130 135
 Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu 155
 145 150
 Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg 170
 160 165
 Thr Ser Thr His Pro Glu Ser Thr
 175 180

<210> 21
 <211> 734
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> (53)...(127)

<221> mat_peptide
 <222> (128)...(655)

<221> CDS
 <222> (53)...(655)

<400> 21
 tgggtgacag cctcagagtg tttcttcgtc tgacaaaagac cagagatcag ga atg aaa 58

Met Lys
-25

cta gac atg acc ggg gac tgc atg cca gtg ctg gtg ctg atg gcc gca	106
Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala	
-20	-15
gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct	154
Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala	
-5	1
5	
ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct	202
Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser	
10	15
20	25
cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag	250
Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu	
30	35
40	
tcg ctt ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg	298
Ser Leu Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg	
45	50
55	
acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg	346
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu	
60	65
70	
gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac	394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp	
75	80
85	
act gac cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg	442
Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu	
90	95
100	105
cac cat atc ctc tcc cag ctc cgg gcc tgt atc cag cct cag ccc acg	490
His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr	
110	115
120	
gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg cac cgg ctc	538
Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His Arg Leu	
125	130
135	
cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc	586
Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val	
140	145
150	
acc tt _c aac ctc ttc cgc ctc acg cga gac ctg aat tgt gtt gcc	634
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala	
155	160
165	
agc ggg gac ctg tgt gtc tga cccttccgcc agtcatgcaa cctgagattt	685
Ser Gly Asp Leu Cys Val *	
170	175
tatttataaa ttagccactt ggcttaattt attgccaccc agtcgctat	734

<210> 22

<211> 200

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> (1)...(25)

<400> 22
 Met Lys Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met -10
 -25 -20 -15
 Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg 5
 -5 -1 -5
 Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser 20
 10 15 20
 Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu 35
 25 30 35
 Glu Glu Ser Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe 55
 40 45 50
 Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val 70
 60 65
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr 85
 75 80
 Ala Asp Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His 100
 90 95
 Thr Leu His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln 115
 105 110 115
 Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His 135
 120 125 130 135
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala 150
 140 145
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys 165
 155 160 165
 Val Ala Ser Gly Asp Leu Cys Val 175
 170 175

<210> 23
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28A mutant C48S

<221> CDS
<222> (1)...(528)

<400> 23 48
 gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 15
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys 1
 5 10 15
 cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe 20 25 30
 aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tcc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp Ser 35 40 45
 agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu 50 55 60
 cag gtg agg gag cgc ccc atg gct ttg gag gac act gac cca gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr 65 70 75 80
 ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp 85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc	336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe	
100 105 110	
cg ^g gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cg ^g ggc	384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly	
115 120 125	
cgc ctc cac cat tgg ctg tac cg ^g ctc cag gag gcc cca aaa aag gag	432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu	
130 135 140	
tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cg ^c ctc	480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu	
145 150 155 160	
ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga	528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *	
165 170 175	

<210> 24
 <211> 175
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> IL-28A mutant C48S

 <400> 24
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser
 35 40 45
 Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 25
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C49S

<221> CDS

<222> (1)...(531)

<400> 25
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
35 40 45
tcc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg 288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85 90 95
gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc 528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175
tga 531
*

<210> 26

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> met IL-28A mutant C49S

<400> 26

Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30

Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 27

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-28A mutant C50S

<221> CDS

<222> (1)...(528)

<400> 27

gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
 35 40 45

agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60

cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
 100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125

cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag 432

Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgcc ctc 480
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga 528
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
 165 170 175

<210> 28

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-28A mutant C50S

<400> 28
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp Cys
 35 40 45
 Arg Ser His Ser Arg Leu Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Phe
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 29

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> met IL-28A mutant C51S

<221> CDS

<222> (1)...(531)

<400> 29

atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp	35	40	45	144
tgc agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	50	55	60	192
ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu	65	70	75	80
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val	85	90	95	288
gac gtc ttg gag cag ccc ctt cac acc ctg cac cat atc ctc tcc cag Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln	100	105	110	336
ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg	115	120	125	384
ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys	130	135	140	432
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg	145	150	155	480
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val	165	170	175	528
tga				531
*				
<210> 30				
<211> 176				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> met IL-28A mutant C51S				
<400> 30				
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly				
1 5 10 15				
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala				
20 25 30				
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp				
35 40 45				
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln				
50 55 60				
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu				
65 70 75 80				
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val				
85 90 95				
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln				
100 105 110				

Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 31
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<221> CDS
<222> (1).....(546)

<400> 31
 ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aaa gct cgt gac gct ctg gaa tct ctg aaa ctg aaa aac tgg tct 144
 Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtt cgt gaa cgt ccg gtt gct ctg gaa gct gct ctg gct ctg acc ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aaa gtt ctg gaa gct gca ggt cct gct ctg gaa gat gtt ctg gat 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccg ctg cac act ctg cac atc ctg tct cag ctg cag gct tgc 336
 Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt ctg cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr
 165 170 175

cat ccg gaa tct acc taa
 His Pro Glu Ser Thr *
 180

<210> 32
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<400> 32
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His
1 5 10 15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
35 40 45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
50 55 60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65 70 75 80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
85 90 95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
100 105 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
115 120 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
130 135 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145 150 155 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr
165 170 175
His Pro Glu Ser Thr
180

<210> 33
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-29 mutant C172S

<221> CDS
<222> (1)...(549)

<400> 33
atg ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
1 5 10 15
cac atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	192
50 55 60	
cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Leu Ala Leu Thr	240
65 70 75 80	
ctg aaa gtt ctg gaa gct gca ggt cct gct ctg gaa gat gtt ctg Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	288
85 90 95	
gat cag ccg ctg cac act ctg cac atc ctg tct cag ctg cag gct Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	336
100 105 110	
tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	384
115 120 125	
cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	432
130 135 140	
ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	480
145 150 155 160	
cgt gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser	528
165 170 175	
acc cat ccg gaa tct acc taa Thr His Pro Glu Ser Thr *	549
180	

<210> 34
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-29 mutant C172S

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys 1 5 10 15	
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe 20 25 30	
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp 35 40 45	
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu 50 55 60	
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr 65 70 75 80	
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu 85 90 95	
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala 100 105 110	
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu 115 120 125	
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala 130 135 140	
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	

<210> 35
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-28A

<221> CDS
<222> (1)...(531)

<400> 35 atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45

tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 19
 Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro' Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cg
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc
Glu Ser Pro Gly Cys Leu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga

* 8

<210> 36
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A

<400> 36
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85 90 95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 37
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-29

<221> CDS
<222> (1)...(549)

<400> 37
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
1 5 10 15
cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
cag gtg agg gag cgcc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga caccccacac cttatttatcg cgctgagccc 579
 Thr His Pro Glu Ser Thr *
 180

tactccctcc-ttaattttt-tcctctcacc-ctttatttat-ga 621

<210> 38
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-29

<400> 38
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr

<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28B

<400> 40
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45
Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 41
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Cys15 mutant, Asn169

<221> CDS
<222> (1)...(546)

<221> variation
<222> (44)...(45)
<223> n = A, T, G, or C

<400> 41
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa His
1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Asn Trp Ser
35 40 45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
50 55 60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240

Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 atc cag cct cag ccc aca gca ggg ccc agg ccc cg^g cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Leu His
 115 120 125
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180
 <210> 42
 <211> 181
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> IL-29 Cys15 mutant, Asn169
 <221> VARIANT
 <222> (15)...(15)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn
 <400> 42
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 43
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Mét IL-29 Cys16 mutant, Asn170

<221> CDS
<222> (1)...(549)

<221> variation
<222> (47)...(48)
<223> n = A; T; G, or C

<400> 43
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa
 1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct gtc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cggt ggc cgc ctc 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175

549

acc cac cct gag tcc acc tga
 Thr His Pro Glu Ser Thr *
 180

<210> 44
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL-29 Cys16 mutant, Asn170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 44
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 45
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Cys15 mutant, Asp169

<221> CDS
<222> (1)...(546)

<221> variation
<222> (44)...(45)
<223> n = A, T, G, or C

<400> 45
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag	96		
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys			
20	25	30	
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt	144		
Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser			
35	40	45	
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag	192		
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln			
50	55	60	
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gac ctg acg ctg	240		
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu			
65	70	75	80
aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta gac	288		
Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp			
85	90	95	
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt	336		
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys			
100	105	110	
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac	384		
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His			
115	120	125	
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc	432		
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly			
130	135	140	
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga	480		
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg			
145	150	155	160
gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc	528		
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr			
165	170	175	
cac cct gag tcc acc tga	546		
His Pro Glu Ser Thr *			
180			

<210> 46

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Cys15 mutant, Asp169

<221> VARIANT

<222> (15)...(15)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 46

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa His			
1	5	10	15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys			
20	25	30	
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser			
35	40	45	
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Gln			

50	55	60	
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu			
65	70	75	80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp			
85	90	95	
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys			
100	105	110	
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His			
115	120	125	
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly			
130	135	140	
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg			
145	150	155	160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr			
165	170	175	
His Pro Glu Ser Thr			
180			

<210> 47
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-29 Cys16 mutant, Asp170

<221> CDS
<222> (1)...(549)

<221> variation

<222> (47)...(48)

<223> n = A, T, G, or C

<400> 47
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa
1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu

115	120	125	
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala			432
130	135	140	
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr			480
145	150	155	160
cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser			528
165	170	175	
acc cac cct gag tcc acc tga Thr His Pro Glu Ser Thr *			549
180			

<210> 48
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL-29 Cys16 mutant, Asp170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 49
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Asp169 Cys171 mutant

<221> CDS
 <222> (1)...(546)

<221> variation.

<222> (512)...(513)

<223> n = A, T, G, or C

<400> 49

ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His
 1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Asn Trp Ser
 35 40 45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 50

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Asp169 Cys171 mutant

<221> VARIANT

<222> (171)...(171)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 50

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Gly	Lys	Gly	Cys	His	
1				5				10				15			
Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	Lys
				20				25				30			
Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Asn	Trp	Ser	
				35				40				45			
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln
				50				55				60			
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu
				65				70				75			80
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp
								85				90			95
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Ala	Cys	
								100				105			110
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His
								115				120			125
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly
								130				135			140
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg
								145				150			160
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Xaa	Leu	Arg	Thr	Ser	Thr
									165				170		175
His	Pro	Glu	Ser	Thr											
				180											

<210> 51

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp170 Cys172 mutant

<221> CDS

<222> (1)...(549)

<221> variation

<222> (515)...(516)

<223> n = A, T, G, or C

<400> 51

atg	ggc	cct	gtc	ccc	act	tcc	aag	ccc	acc	aca	act	ggg	aag	ggc	tgc
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Gly	Lys	Gly	Cys	
1								5							15

cac	att	ggc	agg	ttc	aaa	tct	ctg	tca	cca	cag	gag	cta	gcg	agc	ttc
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe
								20							30

aag	aag	gcc	agg	gac	gcc	ttg	gaa	gag	tca	ctc	aag	ctg	aaa	aac	tgg
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp
								35				40			45

agt	tgc	agc	tct	cct	gtc	ttc	ccc	ggg	aat	tgg	gac	ctg	agg	ctt	ctc
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu
								50				55			60

cag	gtg	agg	gag	cgc	cct	gtg	gcc	ttg	gag	gct	gag	ctg	gcc	ctg	acg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175
 acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180
 <210> 52
 <211> 182
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Met IL-29 Asp170 Cys172 mutant
 <221> VARIANT
 <222> (172)...(172)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn
 <400> 52
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 53
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Asn169 Cys171 mutant

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (30)...(30)
 <223> n = A, T, G, or C

<221> variation
 <222> (512)...(513)
 <223> n = A, T, G, or C

<400> 53
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1 5 10 15
 att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga
His Pro Glu Ser Thr *
180

<210> 54
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29_Pro10_Asn169_Cys171-mutant

<221> VARIANT
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 54
 Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 55
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met_IL-29_Pro11_Asn170_Cys172 mutant

<221> CDS
<222> (1) ... (549)

<221> variation
<222> 33, 515, 516
<223> n = A, T, G, or C

<400> 55

atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 56
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met .IL-29 Pro11 Asn170 Cys172 mutant

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 56
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe

20	25	30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp		
35	40	45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu		
50	55	60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr		
65	70	75
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu		
85	90	95
Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala		
100	105	110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu		
115	120	125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala		
130	135	140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr		
145	150	155
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser		
165	170	175
Thr His Pro Glu Ser Thr		
180		

<210> 57
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Pro10 Cys15 mutant Asn169

<221> CDS
<222> (1) . . . (546)

<221> variation
<222> (30)...(30)
<223> n = A, T, G, or C

<221> variation
<222> (44) ... (45)
<223> n = A, T, G, or C

<400> 57 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30

144

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt	Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser		
	35	40	45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

50
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65 70 75 80

aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta gac 288
Iys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp

85	90	95	
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys 100	105	110	336
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His 115	120	125	384
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly 130	135	140	432
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg 145	150	155	480
gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr 165	170	175	528
cac cct gag tcc acc tga His Pro Glu Ser Thr * 180			546
<210> 58			
<211> 181			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> IL-29 Pro10 Cys15 mutant Asn169			
<221> VARIANT			
<222> (15)...(15)			
<223> Xaa = Ser, Ala, Thr, Val, or Asn			
<400> 58			
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His 1 5 10 15			
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys 20 25 30			
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser 35 40 45			
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln 50 55 60			
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu 65 70 75 80			
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp 85 90 95			
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys 100 105 110			
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His 115 120 125			
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly 130 135 140			
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg 145 150 155 160			
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr 165 170 175			
His Pro Glu Ser Thr 180			

<210> 59
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-29 Pro11 Cys16 mutant Asn170

<221> CDS
<222> (1) . . . (549)

<221> variation
<222> (33) ... (33)
<223> n = A, T, G, C

<221> variation

<222> (47) . . . (48)

<223> n = A, T, G, or C

<400> 59
atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cg_g ggc cgc ccc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 460
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acy tca
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 . 170 . 175

acc cac cct gag tcc acc tga
 Thr His Pro Glu Ser Thr *
 180

<210> 60
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met IL-29 Pro11 Cys16 mutant Asn170

<221> VARIANT
 <222> (16)...(16)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 60
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 61
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Pro10 Asp169 Cys171 mutant

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (30)...(30)
 <223> n = A, T, G, or C

<221> variation
 <222> (512)...(513)
 <223> n = A, T, G, or C

<400> 61
 ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac 48

Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1 5 10 15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Asn Trp Ser
 35 40 45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Ala Cys
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 62
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 Pro10 Asp169 Cys171 mutant

<221> VARIANT
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 62
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1 5 10 15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 63
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-29 Pro11 Asp170 Cys172 mutant

<221> CDS
<222> (1)...(549)

<221> variation
<222> (33)...(33)
<223> n = A, T, G, or C
<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 63
atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cg^g ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn c^ttg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr
 180

<210> 64
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL-29 Pro170 Cys172 mutant

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 64
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60 65
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 65
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Pro10 Cys15 mutant Asp169

<221> CDS
<222> (1)...(546)

<221> variation
<222> 30, 44, 45
<223> n = A, T, G, or C

<400> 65	48
ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac	
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His	
1 5 10 15	
att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag	96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys	
20 25 30	
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt	144
Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser	
35 40 45	
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag	192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln	
50 55 60	
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg	240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu	
65 70 75 80	
aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac	288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp	
85 90 95	
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt	336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Ala Cys	
100 105 110	
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac	384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His	
115 120 125	
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc	432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly	
130 135 140	
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga	480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg	
145 150 155 160	
gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc	528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr	
165 170 175	
cac cct gag tcc acc tga	546
His Pro Glu Ser Thr *	
180	

<210> 66
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 Pro10 Cys15 mutant Asp169

<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 66
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
1 5 10 15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
35 40 45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
50 55 60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65 70 75 80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
85 90 95
Gln Pro Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
100 105 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
115 120 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
130 135 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145 150 155 160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
165 170 175
His Pro Glu Ser Thr
180

<210> 67
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-29 Pro11 Cys16 mutant Asp170

<221> CDS
<222> (1)...(549)

<221> variation
<222> 33, 47, 48
<223> n = A, T, G, or C

<400> 67
atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
1 5 10 15
cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp

35

40

45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 68

<211> 182

<212> PRT

<213> Artificial Sequence

<220>
<223> Met IL-29 Pro11 Cys16 mutant Asp170

<221> VARIANT

<222> (16)...(16)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 68
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala

100	105	110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu		
115	120	125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala		
130	135	140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr		
145	150	155
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser		
165	170	175
Thr His Pro Glu Ser Thr		
180		

<210> 69

<211> 546

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 Asp18 Asn169 Cys171 mutant

<221> CDS

<222> (1)...(546)

<221> variation

<222> (512)...(513)

<223> n = A, T, G, or C

<400> 69	48		
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac			
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His			
1	5	10	15

att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag	96		
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys			
20	25	30	

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt	144		
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser			
35	40	45	

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag	192		
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln			
50	55	60	

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg	240		
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu			
65	70	75	80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac	288		
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp			
85	90	95	

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt	336		
Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala Cys			
100	105	110	

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac	384		
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His			
115	120	125	

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc	432		
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly			
130	135	140	

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aac ctg dnn aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 70

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Asp18 Asn169 Cys171 mutant

<221> VARIANT

<222> (171) ... (171)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 70

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Gly	Gly	Cys	His		
1							10			15					
Ile	Asp	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	Lys
	20						25			30					
Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser
	35					40				45					
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln
	50				55				60						
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu
	65				70				75					80	
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp
	85					90				95					
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys
	100					105				110					
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His
	115					120				125					
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly
	130					135				140					
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg
	145					150				155				160	
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asn	Leu	Xaa	Leu	Arg	Thr	Ser	Thr
	165								170				175		
His	Pro	Glu	Ser	Thr											
	180														

<210> 71

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp19 Asn170 Cys172 mutant

<221> CDS

<222> (1) ... (549)

<221> variation

<222> (515) ... (516)

<223> n = A, T, G, or C

<400> 71 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15

cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta 28
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cg_g ggc cg_c ctc 38
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

150 ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 48
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 155 160

145 150
cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 51
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
165 170 175

105
acc cac cct gag tcc acc tga
Thr His Pro Glu Ser Thr *
106

<210> 72

<210> 72
<211> 182

<211> 182
<212> PRT

<212> PRI
<213> Artificial Sequence

<220>

<223> Met

<221> VARIANT

<223> Xaa = S

<400> 72

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 73
 <211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-29 Cys15 mutant Asp18 Asn169

<221> CDS
 <222> (1)...(546)

<221> variation
 <222> (44)...(45)
 <223> n = A, T, G, or C

<400> 73
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta gac 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cac cgg ctc cag gag ggc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acc tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175

cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 74

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Cys15 mutant Asp18 Asn169

<221> VARIANT

<222> (15)...(15)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 74

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1 5 10 15

Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45

Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95

Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
 165 170 175

His Pro Glu Ser Thr
 180

<210> 75
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-29 Cys16 mutant Asp19 Asn170

<221> CDS
<222> (1)...(549)

<221> variation
<222> (47)...(48)
<223> n. = A, T, G, or C

<400> 75
atg ggc cct gtc ccc act tcc aag ccc acc acal act ggg aag ggc dnn 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa
1 5 10 15

cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
165 170 175

acc cac cct gag tcc acc tga
Thr His Pro Glu Ser Thr *
180

<210> 76
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL-29 Cys16 mutant Asp19 Asn170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 76
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa
1 5 10 15
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 77
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Asp18 Asp169 Cys171 mutant

<221> CDS
<222> (1)...(546)

<221> variation
<222> (512)...(513)
<223> n = A, T, G, or C

<400> 77
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His
1 5 10 15
att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser

35	40	45	
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln			192
50	55	60	
gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu			240
65	70	75	80
aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta gac Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp			288
85	90	95	
cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys			336
100	105	110	
atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Gly Arg Leu His			384
115	120	125	
cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly			432
130	135	140	
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg			480
145	150	155	160
gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr			528
165	170	175	
cac cct gag tcc acc tga His Pro Glu Ser Thr *			546
180			
<210> 78			
<211> 181			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> IL-29 Asp18 Asp169 Cys171 mutant			
<221> VARIANT			
<222> (171)...(171)			
<223> Xaa = Ser, Ala, Thr, Val, or Asn			
<400> 78			
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His			
1 5 10 15			
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys			
20 25 30			
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser			
35 40 45			
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln			
50 55 60			
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu			
65 70 75 80			
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp			
85 90 95			
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys			

	100	105	110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His			
	115	120	125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly			
	130	135	140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg			
	145	150	155
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr			
	165	170	175
His Pro Glu Ser Thr			
	180		

<210> 79

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-29 Asp19 Asp170 Cys172 mutant

<221> CDS

<222> (1)...(549)

<221> variation

<222> (515)...(516)

<223> n = A, T, G, or C

<400> 79

atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc	48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys	
1 5 10 15	

cac att gay agg ttc aaa tct ctg tca cca ca ^g gag cta gc ^g agc ttc	96
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe	
20 25 30	

aag aag gcc agg gac gcc ttg ga ^a gag tca ctc aag ctg aaa aac tgg	144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp	
35 40 45	

agt tgc agc tct cct gtc tt ^c ccc ggg aat tgg gac ctg agg ctt ctc	192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg	240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	

ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta	288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc	336
Asp Gln Pro Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115 120 125	

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct	432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130 135 140	

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 80

<211> 182

<212> PRT

<213> Artificial Sequence

<220>
 <223> Met IL-29 Asp19 Asp170 Cys172 mutant

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 80
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 81

<211> 546

<212> DNA

<213> Artificial Sequence

<220>
 <223> IL-29 Cys15 mutant Asp18 Asp169

<221> CDS

<222> (1)...(546)

<221> variation

<222> (44)...(45)

<223> n = A, T, G, or C

<400> 81
 ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac 48
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag 96
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Asn Trp Ser
 35
 tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gag 288
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt 336
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac 384
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc 432
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga 480
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc 528
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 cac cct gag tcc acc tga 546
 His Pro Glu Ser Thr *
 180

<210> 82
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 Cys15 mutant Asp18 Asp169

<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 82

Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa His
 1 5 10 15
 Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80
 Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
 85 90 95
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160
 Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
 165 170 175
 His Pro Glu Ser Thr
 180

<210> 83
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-29 Cys16 mutant Asp19 Asp170

<221> CDS
<222> (1) ... (549)

<221> variation
<222> (47) ... (48)
<223> n = A, T, G, or C

<400> 83 48
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cg^g ggc cgc ctc 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
 165 170 175

acc cac cct gag tcc acc tga 549
 Thr His Pro Glu Ser Thr *
 180

<210> 84

<211> 182

<212> PRT

<213> Artificial Sequence

<220>
<223> Met IL-29 Cys16 mutant Asp19 Asp170

<221> VARIANT

<222> (16)...(16)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 84
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Xaa
 1 5 10 15
 His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 85
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28B Cys48 mutant
<221> CDS
<222> (1)...(528)

<221> variation
<222> (143)...(144)
<223> n = A, T, G, or C

<400> 85	48
gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc	
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys	
1 5 10 15	
cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt	96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe	
20 25 30	
aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn	144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Xaa	
35 40 45	
aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg	192
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu	
50 55 60	
cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg	240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	
ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat	288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp	
85 90 95	
gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc	336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu	
100 105 110	
cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc	384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly	
115 120 125	
cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag	432
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu	
130 135 140	
tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc	480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu	
145 150 155 160	
ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga	528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *	
165 170 175	

<210> 86
<211> 175
<212> PRT

<213> Artificial Sequence

<220>

<223> IL-28B Cys48 mutant

<221> VARIANT

<222> (48) . . . (48)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 86
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
 35 40 45
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 87

<211> 531

<212> DNA

<213> Artificial Sequence

<220>

<223> Met IL-28B Cys49 mutant

<221> CDS

<222> (1) . . . (531)

<221> variation

$\langle 222 \rangle$ (146) . . . (147)

<223> n = A, T, G, or C

<400> 87

atg gtt cct gtc gcc agg ctc tgc ggg gct ccc ttt 5
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala.
 20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45

dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag 432
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga 531
 *

<210> 88
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Met IL-28B Cys49 mutant
 <221> VARIANT
 <222> (49)...(49)
 <223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 88
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val.
 165 170 175

<210> 89
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28B Cys50 mutant

<221> CDS
 <222> (1) ... (528)

<221> variation

<222> (149) ... (150)

<223> n = A, T, -G, or C

<400> 89
 gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp Cys
 35 40 45

aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60

cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat 288
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125

cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag 432
 Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc acg ggg gac ctg tgt gtc tga 528
 *
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 90
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-28B Cys50 mutant

<221> VARIANT
<222> (50)...(50)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 90
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
1 5 10 15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
35 40 45
Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly ASP
85 90 95
Val Leu Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu
100 105 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
115 120 125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
130 135 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145 150 155 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 91
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-28B Cys51 mutant

<221> CDS
<222> (1)...(531)

<221> variation
<222> (152)...(153)
<223> n = A, T, G, or C

<400> 91
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
5 10 15
tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144

Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp					
35	40	45			
tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag					192
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln					
50	55	60			
ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg					240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu					
65	70	75			80
acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg					288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly					
85	90	95			
gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag					336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln					
100	105	110			
ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg					384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg					
115	120	125			
ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag					432
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys					
130	135	140			
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc					480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg					
145	150	155			160
ctc ctc acg cga gac ctg aat tgt gtt gcc acg ggg gac ctg tgt gtc					528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val					
165	170	175			
tga					531

*
<210> 92
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL-28B Cys51 mutant.
<221> VARIANT
<222> (51)...(51)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 92
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
35 40 45
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95

Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175
 160

<210> 93
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28B Cys48 mutant T87S H135Y

<221> CDS
<222> (1)...(528)

<221> variation
<222> 143, 144, 261
<223> n = A, T, G, or C

<400> 93
gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
1 5 10 15
1 5 10 15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn 144
Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp Xaa
35 40 45

aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50 55 60

cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat 288
Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
115 120 125

cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag 432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480

Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu	160	
145	150	155
ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga	528	
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *		
165	170	175

<210> 94
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (48)...(48)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (87)...(87)
<223> Xaa = Ser

<400> 94
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp Xaa
 35 40 45
 Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 95
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-28B Cys49 mutant T88S H136Y

<221> CDS
<222> (1) ... (531)

<221> variation
<222> 146, 147, 264
<223> n = A, T, G, or C

<400> 95 atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45

dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 . 50 . 55 . 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80

acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg 288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cg 384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125

gac cgc ctc cac cat tgg ctg tay cggt ctc cag gag gcc cca aaa aag 431
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgcc 48
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160

145 ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 52
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

tga * 351

<210> 96
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (49)...(49)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (136) ... (136)
<223> Xaa = Ser

<223> Met IL-28B Cys49 mutant T88S H136Y

<400> 96

Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 97

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-28B Cys50 mutant T87S H135Y

<221> CDS

<222> (1)...(528)

<221> variation

<222> 149, 150, 261

<223> n = A, T, G, or C

<400> 97

gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
 Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
 35 40 45

aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
 Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60

cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat 288
 Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
 85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu 100	105	110	336
cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly 115	120	125	384
cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu 130	135	140	432
tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu 145	150	155	480
ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val 165	170	175	528

<210> 98
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (50)...(50)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (87)...(87)
<223> Xaa = Ser
<223> IL-28B Cys50 mutant T87S H135Y

<400> 98			
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys			
1	5	10	15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe			
20	25	30	
Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp Cys			
35	40	45	
Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu			
50	55	60	
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr			
65	70	75	80
Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp			
85	90	95	
Val Leu Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu			
100	105	110	
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly			
115	120	125	
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu			
130	135	140	
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu			
145	150	155	160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val			
165	170	175	

<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-28B Cys51 mutant T88S H136Y

<221> CDS
<222> (1)...(531)

<221> variation

<222> 152, 152, 264
<223> n = A, T, G, or C

<400> 99
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45

tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80

acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg 288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125

ggc cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

531

tga

*

<210> 100

<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (51)...(51)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (88)...(88)
<223> Xaa = Ser

<223> Met IL-28B Cys51 mutant T88S H136Y

<400> 100
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
35 40 45
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 101
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> signal sequence

<221> CDS
<222> (1)...(45)

<221> variation
<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45
<223> n = A, T, G, or C

<400> 101
atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn 45
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly
1 5 10 15

<210> 102
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 102

Met Ala Ala Ala Trp Thr Val Val Val Leu Val Thr Leu Val Leu Gly

1 5 10 15

<210> 103

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> signal sequence

<221> CDS

<222> (1)...(57)

<221> variation

<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,

54, 57

<223> n = A, T, G, or C

<400> 103

atg gcn gcn gcn tgg acn gtn gtn ytn gtn acn ytn gtn ytn ggn ytn 48

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu

1 5 10 15

57

gcn gtn gcn

Ala Val Ala

<210> 104

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 104

Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu

1 5 10 15

Ala Val Ala

<210> 105

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> signal sequence

<221> CDS

<222> (1)...(63)

<221> variation

<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,

54, 57, 60, 63

<223> n = A, T, G, or C

<400> 105
atg gcn gcn gcn tgg acn gtn gtn ytn acn ytn gtn ytn ggn ytn 48
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
1 5 10 15
gcn gtn gcn ggn ccn 63
Ala Val Ala Gly Pro
20

<210> 106

<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<400> 106
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu 15
1 5 10
Ala Val Ala Gly Pro
20

<210> 107

<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> signal sequence

<221> CDS
<222> (1)...(72)

<221> variation
<222> 6, 9, 12, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51,
54, 57, 60, 63, 66, 69, 72
<223> n = A, T, G, or C

<400> 107
atg gcn gcn gcn tgg acn gtn gtn ytn acn ytn gtn ytn ggn ytn 48
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
1 5 10 15
gcn gtn gcn ggn ccn gtn ccn acn 72
Ala Val Ala Gly Pro Val Pro Thr
20

<210> 108

<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<400> 108
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu 15
1 5 10
Ala Val Ala Gly Pro Val Pro Thr

<210> 109
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C171X

<221> CDS
<222> (1) . . . (546)

<221> variation
<222> (512)...(513)
<223> n = A, T, G, or C

<400> 109 ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac 48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His
1 5 10 15

atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
20 25 30

aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct 144
 Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
 35 40 45

tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag 192
 Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
 50 55 60

gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg 240
 Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65 70 75 80

aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat 288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
85 90 95

cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc
 Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
 100 105 110

att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac 38
 Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
 115 120 125

cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt 43
 His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
 130 135 140

tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt cgt ctg ctg acc acc cgt 48
 Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
 145 150 155 160

gat ctg aaa tac gtt gct gat ggt aac ctg dnn ctg cgt acc tct acc 52
 Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
 165 170 175

cat ccg gaa tct acc taa 54
His Pro Glu Ser Thr *

180

<210> 110
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 C171X

<221> VARIANT

<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 110 D Pro Thr Thr Thr Gly Iys Gly Cys His

Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys	Mis
1				5					10					15	
Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe	Lys
								20		25				30	
Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser
								35		40				45	
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln
								50		55				60	
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu
								65		70				75	
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp
								85			90			95	
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys
								100			105			110	
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His
								115		120				125	
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly
								130		135				140	
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg
								145			155			160	
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asn	Leu	Xaa	Leu	Arg	Thr	Ser	Thr
								165		170				175	
His	Pro	Glu	Ser	Thr											
								180							

<210> 111
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-29 C172X

<221> CDS
<222> (1)...(549)

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 111 atg ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc 48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15

cac atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

aaa aaa gct cgt gac gct ctg gaa tct ctg aaa ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

tct tgc tct tct ccg gtt ttcc cg ggt aac tgg gat ctg cgt ctg ctg 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aaa gtt ctg gaa gct gca ggt cct gct ctg gaa gat gtt ctg 288
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95

gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cgt gat ctg aaa tac gtt gct gat ggt aac ctg dnn ctg cgt acc tct 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175

acc cat ccg gaa tct acc taa 549
 Thr His Pro Glu Ser Thr *
 180

<210> 112

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Met IL-29 C172X

<221> VARIANT

<222> (172)...(172)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 112

Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
 1 5 10 15

His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30

Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60

Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
 165 170 175
 Thr His Pro Glu Ser Thr
 180

<210> 113

<211> 543

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C170X, truncated after N-terminal Methionine
and Glycine

<221> CDS

<222> (1) ... (543)

<221> variation

<222> (509) ... (510)

<223> n = A, T, G, or C

<400> 113

cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att 48
 Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile
 1 5 10 15

ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag 96
 Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys
 20 25 30

gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc 144
 Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Asn Trp Ser Cys
 35 40 45

agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg 192
 Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val
 50 55 60

agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag 240
 Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys
 65 70 75 80

gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag 288
 Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln
 85 90 95

ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc 336
 Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile
 100 105 110

cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac 384
 Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His
 115 120 125

tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc 432
Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys
130 135 140

ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg cga gac 480...
Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp
145 150 155 160

ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac 528
Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His
165 170 175

cct gag tcc acc tga 543
Pro Glu Ser Thr *
180

<210> 114

<211> 180

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 C170X, truncated after N-terminal Methionine
and Glycine

<221> VARIANT

<222> (170)...(170)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 114
Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile
1 5 10 15
Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys
20 25 30
Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys
35 40 45
Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val
50 55 60
Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys
65 70 75 80
Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln
85 90 95
Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile
100 105 110
Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His
115 120 125
Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys
130 135 140
Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp
145 150 155 160
Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His
165 170 175

Pro Glu Ser Thr
180

<210> 115

<211> 540

<212> DNA

<213> Artificial Sequence

<220>
<223> IL-29 C169X, truncated after N-terminal

Methionine, Glycine, and Proline

<221> CDS
 <222> (1)...(540)

<221> variation

<222> (506)...(507)

<223> n = A, T, G, or C

<400> 115 48
 gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc
 Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly
 10 15
 1 5

agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc 96
 Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala
 20 25 30

agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc 144
 Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser
 35 40 45

tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg 192
 Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg
 50 55 60

gag cgc cct gtg gcc ttg gag gct gag ctg gac ctg acg ctg aag gtc 240
 Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val
 65 70 75 80

ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta gac cag ccc 288
 Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro
 85 90 95

ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag 336
 Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln
 100 105 110

cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg 384
 Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp
 115 120 125

ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg 432
 Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu
 130 135 140

gag gca tct gtc acc ttc aac ctc ttc cgc ctc acg cga gac ctc 480
 Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
 145 150 155 160

aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct 528
 Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro
 165 170 175

540

gag tcc acc tga
 Glu Ser Thr *

<210> 116

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 C169X, truncated after N-terminal
Methionine, Glycine, and Proline

<221> VARIANT

<222> (169)....(169)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 116
Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly
1 5 10 15
Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala
20 25 30
Arg Asp Ala Leu Glu Glu Ser Leu Lys Lys Asn Trp Ser Cys Ser
35 40 45
Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg
50 55 60
Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val
65 70 75 80
Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro
85 90 95
Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln
100 105 110
Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp
115 120 125
Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu
130 135 140
Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
145 150 155 160
Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro
165 170 175
Glu Ser Thr

<210> 117

<211> 537

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C168X, truncated after N-terminal
Methionine, Glycine, Proline, and Valine

<221> CDS

<222> (1)...(537)

<221> variation

<222> (503)...(504)

<223> n = A, T, G, or C

<400> 117
ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg
1 5 10 15
Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg

48

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg
20 25 30
Phe Lys Ser Leu Ser Pro Gln Glu Ala Ser Phe Lys Lys Ala Arg

96

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct
35 40 45
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser

144

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu

192

50	55	60	
cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu 65 70 75 80			240
gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu 85 90 95			288
cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct His Thr Leu His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro 100 105 110			336
cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg Gln Pro Thr Ala Gly Pro Arg Gly Arg Leu His His Trp Leu 115 120 125			384
cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu 130 135 140			432
gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys 145 150 155 160			480
tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu 165 170 175			528
tcc acc tga Ser Thr *			537
<210> 118			
<211> 178			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> IL-29 C168X, truncated after N-terminal Methionine, Glycine, Proline, and Valine			
<221> VARIANT			
<222> (168)...(168)			
<223> Xaa = Ser, Ala, Thr, Val, or Asn			
<400> 118			
Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg 1 5 10 15			
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg 20 25 30			
Asp Ala Leu Glu Glu Ser Leu Lys Asn Trp Ser Cys Ser Ser 35 40 45			
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu 50 55 60			
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu 65 70 75 80			
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu 85 90 95			
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro 100 105 110			
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu 115 120 125			

His Arg Leu Gln Glu Ala Pro Lys Lys Ser Ala Gly Cys Leu Glu
 130 135 140
 Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
 145 150 155 160
 Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu
 165 170 175
 Ser Thr

<210> 119

<211> 534

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29-C167X, truncated after N-terminal
Methionine, Glycine, Proline, Valine, and Proline

<221> CDS

<222> (1)...(534)

<221> variation

<222> (500)...(501)

<223> n = A, T, G, or C

<400> 119

act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc 48
 Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe
 1 5 10 15

aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac 96
 Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp
 20 25 30

gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct 144
 Ala Leu Glu Ser Leu Lys Asn Trp Ser Cys Ser Ser Pro
 35 40 45

gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc 192
 Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Lys Val Arg Glu Arg
 50 55 60

cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag 240
 Pro Val Ala Leu Glu Ala Leu Ala Leu Thr Leu Lys Val Leu Glu
 65 70 75 80

gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac 288
 Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His
 85 90 95

acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag 336
 Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln
 100 105 110

ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac 384
 Pro Thr Ala Gly Pro Arg Gly Arg Leu His His Trp Leu His
 115 120 125

cggtt ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca 432
 Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala
 130 135 140

tct gtc acc ttc aac ctc ttc cgc ctc acg cga gac ctc aaa tat 480
 Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr

145	150	155	160	528
				gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc
				Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser
		165	170	175

acc tga
Thr *

534

<210> 120
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 C167X, truncated after N-terminal
Methionine, Glycine, Proline, Valine, and Proline

<221> VARIANT
<222> (167)...(167)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 120
Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe
15
1 Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp
20 25 30
Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro
35 40 45
Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg
50 55 60
Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu
65 70 75 80
Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His
85 90 95
Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln
100 105 110
Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His
115 120 125
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala
130 135 140
Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr
145 150 155 160
Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser
165 170 175
Thr

<210> 121
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C166X, truncated after N-terminal
Methionine, Glycine, Proline, Valine, Proline, and
Threonine

<221> CDS
<222> (1)...(531)
<221> variation

<222> (497)...(498)

<223> n = A, T, G, or C

<400> 121	48
tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa	
Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys	
5 10 15	
tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc	96
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala	
20 25 30	
ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc	144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val	
35 40 45	
ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgcc cct	192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro	
50 55 60	
gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc	240
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala	
65 70 75 80	
gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc	288
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr	
85 90 95	
ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc	336
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro	
100 105 110	
aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg	384
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg	
115 120 125	
ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct	432
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser	
130 135 140	
gtc acc ttc aac ctc ttc cgc ctc acg cga gac ctc aaa tat gtg	480
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val	
145 150 155 160	
gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc	528
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr	
165 170 175	

531

tga

*

<210> 122
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 C166X, truncated after N-terminal Methionine, Glycine, Proline, Valine, Proline, and Threonine

<221> VARIANT

<222> (166)...(166)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 122
 Ser Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1 5 10 15
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
 20 25 30
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
 35 40 45
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
 50 55 60
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
 85 90 95
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
 100 105 110
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
 115 120 125
 Leu Gln Glu Ala Pro Lys Lys Ser Ala Gly Cys Leu Glu Ala Ser
 130 135 140
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
 145 150 155 160
 Ala Asp Gly Asn Leu Xaa Leu Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 165 170 175

<210> 123

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-29 C165X, truncated after N-terminal
 Methionine, Glycine, Proline, Valine, Proline,
 Threonine, and Serine

<221> CDS

<222> (1)...(528)

<221> variation

<222> (494)...(495)

<223> n = A, T, G, or C

<400> 123
 aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa tct 48
 Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser
 1 5 10 15
 ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc ttg 96
 Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu
 20 25 30
 gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc ttc 144
 Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe
 35 40 45
 ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct gtg 192
 Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val
 50 55 60
 gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc gct 240
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala
 65 70 75 80

288

gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc ctg
 Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu
 85 90 95

336

cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc aca
 His His Ile Leu Ser Gln Leu Ala Cys Ile Gln Pro Gln Pro Thr
 100 105 110

384

gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg ctc
 Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu
 115 120 125

432

cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct gtc
 Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val
 130 135 140

480

acc ttc aac ctc ttc cgc ctc acg cga gac ctc aaa tat gtg gcc
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala
 145 150 155 160

gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc tga
 Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 165 170 175

528

<210> 124

<211> 175

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 C165X, truncated after N-terminal
 Methionine, Glycine, Proline, Valine, Proline,
 Threonine, and Serine

<221> VARIANT

<222> (165)...(165)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 124
 Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser
 1 5 10 15
 Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu
 20 25 30
 Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe
 35 40 45
 Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val
 50 55 60
 Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala
 65 70 75 80
 Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu
 85 90 95
 His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr
 100 105 110
 Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu
 115 120 125
 Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val
 130 135 140
 Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala
 145 150 155 160
 Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 165 170 175

<210> 125
<211> 552
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Leu insert after N-terminal Met, C173X

<221> CDS
<222> (1)...(552)

<221> variation
<222> (6)...(6)
<223> n = A, T, G, or C

<221> variation

<222> (518)...(519)

<223> n = A, T, G, or C

<400> 125 atg ytn ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc 48

Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly 15

1

5

10

15

tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc 96

Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser 20

25

30

ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac 144

Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn 35

40

45

tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt 192

Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu 50

55

60

ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg 240

Leu Gln Val Arg Glu Arg Pro Val Ala Leu Ala Glu Leu Ala Leu 65

70

80

acg ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc 288

Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val 85

90

95

cta gac cag ccc ctt cac acc ctg cac atc ctc tcc cag ctc cag 336

Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln 100

105

110

gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc 384

Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg 115

120

125

ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc 432

Leu His His Trp Leu His Arg Leu Gln Ala Pro Lys Lys Glu Ser 130

135

140

gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc 480

Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu 145

150

155

160

acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg 528

Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr 165

170

175

tca acc cac cct gag tcc acc tga

552

Ser Thr His Pro Glu Ser Thr *
180

<210> 126
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 Leu insert after N-terminal Met, C173X

<221> VARIANT
<222> (173)...(173)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 126
Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly
1 5 10 15
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
20 25 30
Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
35 40 45
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
50 55 60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
85 90 95
Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
100 105 110
Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
115 120 125
Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
130 135 140
Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
145 150 155 160
Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
165 170 175
Ser Thr His Pro Glu Ser Thr
180

<210> 127
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 G2L C172X

<221> CDS
<222> (1)...(549)

<221> variation
<222> (6)...(6)
<223> n = A, T, G, or C

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 127
atg ytn cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc
Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys

1	5	10	15	
cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe				96
20 25				30
aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp				144
35 40				45
agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu				192
50 55				60
cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr				240
65 70				75 80
ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc cta Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu				288
85 90				95
gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala				336
100 105				110
tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg gcc cgc ctc Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu				384
115 120				125
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct His His Trp Leu His Arg Leu Gln Ala Pro Lys Lys Glu Ser Ala				432
130 135				140
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg Gly Cys Leu Glu Ala Ser Val Phe Asn Leu Phe Arg Leu Leu Thr				480
145 150				155 160
cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser				528
165 170				175
acc cac cct gag tcc acc tga Thr His Pro Glu Ser Thr *				549
180				

<210> 128
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 G2L C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 128
Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp

35	40	45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu		
50	55	60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr		
65	70	75
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu		
85	90	95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala		
100	105	110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu		
115	120	125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala		
130	135	140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr		
145	150	155
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser		
165	170	175
Thr His Pro Glu Ser Thr		
180		

<210> 129
<211> 552
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Ile insert after N-terminal Met, C173X

<221> CDS

<222> (1)...(552)

<221> variation

<222> (518)...(519)

<223> n = A, T, G, or C

<400> 129 48
atg ath ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc
Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly
10 15

1 5 96
tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
20 25 30

ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac 144
Phe Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn
35 40 45

tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt 192
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
50 55 60

ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Ala Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80

acg ctg aag gtc ctg gag gcc gct ggc cca gcc ctg gag gac gtc 288
Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val
85 90 95

cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag 336
Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
100 105 110

gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cg_g ggc cgc 384
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
 115 120 125

ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc 432
 Leu His His Trp Leu His Arg Leu Gln Ala Pro Lys Lys Glu Ser
 130 135 140

gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc 480
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
 145 150 155 160

acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg 528
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
 165 170 175

tca acc cac cct gag tcc acc tga 552
 Ser Thr His Pro Glu Ser Thr *
 180

<210> 130

<211> 183

<212> PRT

<213> Artificial Sequence

<220>
<223> IL-29 Ile insert after N-terminal Met, C173X

<221> VARIANT

<222> (173)...(173)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 130
 Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly 15
 1 5 10 15
 Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser 20 25 30
 Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn 35 40 45
 Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val 85 90 95
 Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln 100 105 110
 Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg 115 120 125
 Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser 130 135 140
 Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu 145 150 155 160
 Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr 165 170 175
 Ser Thr His Pro Glu Ser Thr 180

<210> 131

<211> 549

<212> DNA

<213> Artificial Sequence

<220>
<223> IL-29 G2I C172X

<221> CDS
<222> (1) ... (549)

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 131 atg ath cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
1 5 10 15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30

20 144
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

55 agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc 192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60

50 cag gtg agg gag cgccctgtggccttggaggctgagctggccctgacg 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 33
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cg_g ggc cg_c ctc 38
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125

cac cac tgg ctg cac cg_g ctc cag gag gcc ccc aaa aag gag tcc gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser.
 165 170 175

acc cac cct gag tcc acc tga
Thr His Pro Glu Ser Thr *
180

<210> 132

<211> 182

<212> PRT

<212> INT
<213> Artificial Sequence

<220>
<223> IL-29 G2I C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 132
Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 133
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 after N-terminal Met amino acid residues 2-7
deleted, C166X

<221> CDS
<222> (1)...(531)

<221> variation
<222> (497)...(498)
<223> n = A, T, G, or C

<400> 133
atg aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa 48
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
1 5 10 15
tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc 96
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Ala Arg Asp Ala
20 25 30
ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc 144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
35 40 45
ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct 192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro

50

55

60

50
gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc 240
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
65 70 75 80
65

65 gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc 288
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
85 90 95

ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc 336
 -Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
 100 105 110

aca gca ggg ccc agg ccc cg_g ggc cg_c ctc cac cac tgg ctg cac cac cg_g
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
120 125

115 120 115 120 432
ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gc^a tct
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
130 135 140

150 gtc acc ttc aac ctc ttc cgcc tc acg cga gac ctc aaa tat gtg 480
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
155 160

145 150 155 160 165 170 175 180 185 190 195 200
 gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc 52
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr

tga

1

<210> 134

<211> 176

<212> PRT

<213> Artificial Sequence

<220> 2-7
220-225 N-terminal Met amino acid residues

<223> IL-29 after N-terminal Met amino acid deleted, C166X

<221> VARIANT

<222> (166) . . . (166)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 134
 Met Lys Pro Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1 5 10 15
 Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
 20 25 30
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
 35 40 45
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
 50 55 60
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
 85 90 95
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
 100 105 110
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
 115 120 125

Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
 130 135 140
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
 145 150 155 160
 Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 165 170 175

<210> 135

<211> 558

<212> DNA

<213> Artificial Sequence

<220>
 <223> IL-29 Glu, Ala, and Glu inserted after N-terminal
 Met, C175X

<221> CDS

<222> (1) ... (558)

<221> variation

<222> (524) ... (525)

<223> n = A, T, G, or C

<400> 135 48
 atg gar gcn gar ggc cct gtc ccc act tcc aag ccc acc aca acti ggg
 Met Glu Ala Glu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly
 1 5 10 15

aag ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta 96
 Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu
 20 25 30

gcg agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg 144
 Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu
 35 40 45

aaa aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg 192
 Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu
 50 55 60

agg ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg 240
 Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu
 65 70 75 80

gcc ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag 288
 Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu
 85 90 95

gac gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctc cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg 384
 Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg
 115 120 125

ggc cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag 432
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gag tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc 480
 Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctc ctc acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg 528
 Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu
 165 170 175

aga acg tca acc cac cct gag tcc acc tga 558
 Arg Thr Ser Thr His Pro Glu Ser Thr *
 180 185

<210> 136

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-29 Glu, Ala, and Glu inserted after N-terminal
Met, C175X

<221> VARIANT

<222> (175)...(175)

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 136 528
 Met Glu Ala Glu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly
 1 5 10 15
 Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu
 20 25 30
 Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu
 35 40 45
 Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu
 50 55 60
 Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu
 65 70 75 80
 Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg
 115 120 125
 Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu
 165 170 175
 Arg Thr Ser Thr His Pro Glu Ser Thr
 180 185

<210> 137

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> Human IL-28A C2 mutant for expression in E. coli

<221> CDS

<222> (1)...(528)

<221> variation

<222> (146)...(147)

<223> n = A, T, G or C

<400> 137

48

atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 15
 1 5 10 15

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttc aaa cgt gct aaa gac gct ctg gaa tct ctg ctg aaa gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40

dnn cgt tgc cac tct cgt ttc ccg cgt acc tgg gac ctg cgt cag 192
 Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90

gac gtt ctg gac cag ccg ctg cac acc ctg cac atc ctg tct cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 138

<211> 176

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IL-28A C2 mutant for expression in E. coli

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 138
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 15
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45

Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 139

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> Human IL-28A C3 mutant for expression in E. coli

<221> CDS

<222> (1) ... (528)

<221> variation

<222> (152) ... (153)

<223> n = A, T, G or C

<400> 139 48
 atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 5 10 15

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg aaa gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45

tgc cgt dnn cac tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192
 Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa 432
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 140

<211> 176

<212> PRT

<213> Artificial Sequence

<220> Human IL-28A C3 mutant for expression in E. coli

<223> Human IL-28A C3 mutant for expression in E. coli

<221> VARIANT

<222> (51)...(51)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 140
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp
 35 40 45
 Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 141

<211> 528

<212> DNA

<213> Artificial Sequence

<220> Human IL-28B C2 mutant for expression in E. coli

<221> CDS

<222> (1)...(528)

<221> variation

<222> 146, 147, 264

<223> n = A, T, G or C

<400> 141 48
atg gtt ccg gtt cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30

ttc aaa cgt gct aaa gac gct ctg gaa tct ctg ctg ctg aaa gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Leu Lys Asp
35 40 45

dnn aaa tgc cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60

ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg 240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80

acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt 288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110

ctg cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt 384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125

ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa 432
Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 142

<211> 176

<212> PRT

<213> Artificial Sequence

<220>
<223> Human IL-28B C2 mutant for expression in E. coli

<221> VARIANT

<222> (49)...(49)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT

<222> (88)...(88)

<223> Xaa = Thr or Ser

<221> VARIANT

<222> (136)...(136)

<223> Xaa = His or Tyr

<400> 142

Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
 35 40 45
 Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 143

<211> 528

<212> DNA

<213> Artificial Sequence

<220>

<223> Human IL-28B C3 mutant for expression in E. coli

<221> CDS

<222> (1)...(528)

<221> variation

<222> 152, 153, 264

<223> n = A, T, G or C

<400> 143

atg gtt ccg gtt gct cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt 48
 Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg aaa gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Lys Asp
 35 40 45

tgc aaa dnn cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag 192
 Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60

ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg 240
 Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt 288
 Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
 85 90 95

gac gtt ctg gac cag ccg ctg cac acc ctg cac atc ctg tct cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110

ctg cgt gct tgc atc cag ccg cag acc gct ggt ccg cgt acc cgt 384
 Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa 432
 Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt 480
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 144

<211> 176

<212> PRT

<213> Artificial Sequence

<220>
 <223> Human IL-28B C3 mutant for expression in E. coli

<221> VARIANT

<222> (51)...(51)

<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT

<222> (88)...(88)

<223> Xaa = Thr or Ser

<221> VARIANT

<222> (136)...(136)

<223> Xaa = His or Tyr

<400> 144

Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 5 10 15

1 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala

20 25 30

Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp

35 40 45

Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln

50 55 60

Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu

65 70 75 80

Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly

85 90 95

Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln

100 105 110

Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg

115 120 125

Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys

130 135 140

Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 145
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IL-29 C1-mutant for expression in E. coli

<221> CDS
 <222> (1) (549)

<221> variation
 <222> 33, 47, 48, 57
 <223> n = A, T, G or C

<400> 145 48
 atg ggt ccg gtt ccg acc tct aaa cca acc mcn act ggt aaa ggt dnn 15
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa
 1 5 10 15
 cac atc grn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg 288
 Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gat cag ccg ctg cac act ctg cac atc atc ctg tct cag ctg cag gct 336
 Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cgt gat ctg aaa tac gtt gct gat ggt ray ctg tgc ctg cgt acc tct 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Cys Leu Arg Thr Ser
 165 170 175

acc cat ccg gaa tct acc taa
 Thr His Pro Glu Ser Thr *
 180

<210> 146
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-29 C1 mutant for expression in E. coli

<221> VARIANT
<222> (11)...(11)
<223> Xaa = Thr or Pro

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT
<222> (19)...(19)
<223> Xaa = Gly or Asp

<221> VARIANT
<222> (170)...(170)
<223> Xaa = Asn or Asp

<400> 146
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa
1 5 10 15
His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Cys Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 147
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-29 C5 mutant for expression in E. coli

<221> CDS
 <222> (1)...(549)

<221> variation:

<222> 33, 57, 515, 516
 <223> n = A, T, G or C

<400> 147 48
 atg ggt ccg gtt ccg acc tct aaa cca acc mcn-act ggt aaa ggt tgc
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Cys
 5 10 15
 1 5
 cac atc grn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc 96
 His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg 192
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gct gct ctg acc 240
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 ctg aaa gtt ctg gaa gct gca ggt cct gct ctg gaa gat gtt ctg 288
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 gat cag ccg ctg cac act ctg cac atc atc ctg tct cag ctg cag gct 336
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 tgc att caa ccg caa ccg acc gct ggt ccg cgt cgt ggt cgt ctg 384
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct 432
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc 480
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160
 cgt gat ctg aaa tac gtt gct gat ggt ray ctg dnn ctg cgt acc tct 528
 Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Xaa Leu Arg Thr Ser
 165 170 175
 acc cat ccg gaa tct acc taa 549
 Thr His Pro Glu Ser Thr *
 180

<210> 148

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IL-29 C5 mutant for expression in E. coli

<221> VARIANT
<222> (11)...(11)
<223> Xaa = Thr or Pro

<221> VARIANT
<222> (19)...(19)
<223> Xaa = Gly or Asp

<221> VARIANT
<222> (170) ... (170)
<223> Xaa = Asp or Asn

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<210> 149

<211> 531

<212> DNA

<213> Artificial Sequence

<220>
222

<223> Human IL-29 ΔZ/ΔC mutant for *Escherichia coli*

<221> CDS
<222> (1)

<222> (1), . . . (551)

<221> Variation
<222> (497) . . . (

<223> n = A, T, G or C

<400> 149

Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
 20 25 30

ctg gaa gaa tct ctg aaa aac tgg tct tgc tct tct ccg gtt 144.
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
 35 40 45

ttc ccg ggt aac tgg gat ctg cgt ctg cag gtt cgt gaa cgt ccg 192
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
 50 55 60

gtt gct ctg gaa gct gaa ctg gct ctg acc ctg aaa gtt ctg gaa gct 240
 Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
 65 70 75 80

gct gca ggt cct gct ctg gaa gat gtt ctg gat cag ccg ctg cac act 288
 Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
 85 90 95

ctg cac cac atc ctg tct cag ctg cag gct tgc att caa ccg caa ccg 336
 Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
 100 105 110

acc gct ggt ccg ccg cgt ggt cgt ctg cac cac tgg ctg cat cgt 384
 Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
 115 120 125

ctg cag gaa gct ccg aaa aaa gaa tct gct ggt tgc ctg gaa gct tct 432
 Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
 130 135 140

gtt acc ttc aac ctg ttc cgt ctg acc cgt gat ctg aaa tac gtt 480
 Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
 145 150 155 160

gct gat ggt aac ctg dnn ctg cgt acc tct acc cat ccg gaa tct acc 528
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<221> VARIANT

<222> (166)...(166)

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 20 25 30
 Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
 35 40 45
 Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro

50 55 60
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
65 70 75 80
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
85 90 95
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
100 105 110
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
115 120 125
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
130 135 140
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
145 150 155 160
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
165 170 175

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